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OIKE

RAW SEQUENCE LISTING

DATE: 09/25/2001

PATENT APPLICATION: US/09/919,408

TIME: 09:56:50

Input Set : N:\Crf3\RULE60\09919408.txt

Output Set: N:\CRF3\09252001\I919408.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Lemischka, Ihor R.

8 (ii) TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
9 RECEPTORS AND THEIR LIGANDS

11 (iii) NUMBER OF SEQUENCES: 10

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: ImClone Systems Incorporated

15 (B) STREET: 180 Varick Street

16 (C) CITY: New York

17 (D) STATE: New York

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 10014

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/919,408

C--> 29 (B) FILING DATE: 31-Jul-2001

30 (C) CLASSIFICATION:

64 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 07/977,451

34 (B) FILING DATE:

37 (A) APPLICATION NUMBER: US 07/906,397

38 (B) FILING DATE: 26-JUN-1992

41 (A) APPLICATION NUMBER: US PCT/US92/05401

42 (B) FILING DATE: 26-JUN-1992

45 (A) APPLICATION NUMBER: TW 81102961

46 (B) FILING DATE: 15-APR-1992

49 (A) APPLICATION NUMBER: US PCT/US92/02750

50 (B) FILING DATE: 02-APR-1992

53 (A) APPLICATION NUMBER: US 07/813,593

54 (B) FILING DATE: 24-DEC-1991

57 (A) APPLICATION NUMBER: US 07/793,065

58 (B) FILING DATE: 15-NOV-1991

61 (A) APPLICATION NUMBER: US 07/728,913

62 (B) FILING DATE: 28-JUN-1991

65 (A) APPLICATION NUMBER: US 07/679,666

66 (B) FILING DATE: 02-APR-1991

68 (viii) ATTORNEY/AGENT INFORMATION:

69 (A) NAME: Feit, Irving N.

70 (B) REGISTRATION NUMBER: 28,601

71 (C) REFERENCE/DOCKET NUMBER: LEM-3-7P

73 (ix) TELECOMMUNICATION INFORMATION:

74 (A) TELEPHONE: 212-645-1405

ENTERED

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75          (B) TELEFAX: 212-645-2054
78 (2) INFORMATION FOR SEQ ID NO: 1:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 3453 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: double
84          (D) TOPOLOGY: linear
86      (ii) MOLECULE TYPE: cDNA
88      (iii) HYPOTHETICAL: NO
90      (iv) ANTI-SENSE: NO
92      (v) FRAGMENT TYPE: N-terminal
95      (ix) FEATURE:
96          (A) NAME/KEY: mat_peptide
97          (B) LOCATION: 112..3006
99      (ix) FEATURE:
100         (A) NAME/KEY: sig_peptide
101         (B) LOCATION: 31..111
103      (ix) FEATURE:
104         (A) NAME/KEY: CDS
105         (B) LOCATION: 31..3009
108      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
110 GCGGCCTGCG TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC      54
111                               Met Arg Ala Leu Ala Gln Arg Ser
112                               -27   -25                   -20
114 GAC CGG CGG CTG CTG CTG CTT GTT GTT TTG TCA GTA ATG ATT CTT GAG      102
115 Asp Arg Arg Leu Leu Leu Leu Val Val Leu Ser Val Met Ile Leu Glu
116                               -15                   -10                   -5
118 ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT      150
119 Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser
120                               1                   5                   10
122 CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG      198
123 His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met
124       15                   20                   25
126 GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT      246
127 Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser
128       30                   35                   40                   45
130 GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG      294
131 Glu Gly Thr Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly
132                               50                   55                   60
134 TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC      342
135 Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys
136                               65                   70                   75
138 CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT      390
139 Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp
140       80                   85                   90
142 TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG      438
143 Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu
144       95                   100                  105
146 ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC      486

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147	Thr	Gln	Ala	Gly	Glu	Tyr	Leu	Leu	His	Ile	Gln	Ser	Glu	Arg	Ala	Asn	
148	110						115				120					125	
150	TAC	ACA	GTA	CTG	TTC	ACA	GTG	AAT	GTA	AGA	GAT	ACA	CAG	CTG	TAT	GTG	534
151	Tyr	Thr	Val	Leu	Phe	Thr	Val	Asn	Val	Arg	Asp	Thr	Gln	Leu	Tyr	Val	
152				130						135					140		
154	CTA	AGG	AGA	CCT	TAC	TTT	AGG	AAG	ATG	GAA	AAC	CAG	GAT	GCA	CTG	CTC	582
155	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys	Met	Glu	Asn	Gln	Asp	Ala	Leu	Leu	
156				145					150					155			
158	TGC	ATC	TCC	GAG	GGT	GTT	CCG	GAG	CCC	ACT	GTG	GAG	TGG	GTG	CTC	TGC	630
159	Cys	Ile	Ser	Glu	Gly	Val	Pro	Glu	Pro	Thr	Val	Glu	Trp	Val	Leu	Cys	
160			160					165					170				
162	AGC	TCC	CAC	AGG	GAA	AGC	TGT	AAA	GAA	GAA	GGC	CCT	GCT	GTT	GTC	AGA	678
163	Ser	Ser	His	Arg	Glu	Ser	Cys	Lys	Glu	Glu	Gly	Pro	Ala	Val	Val	Arg	
164		175					180				185						
166	AAG	GAG	GAA	AAG	GTA	CTT	CAT	GAG	TTG	TTC	GGA	ACA	GAC	ATC	AGA	TGC	726
167	Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	
168	190					195				200						205	
170	TGT	GCT	AGA	AAT	GCA	CTG	GGC	CGC	GAA	TGC	ACC	AAG	CTG	TTC	ACC	ATA	774
171	Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg	Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	
172				210					215					220			
174	GAT	CTA	AAC	CAG	GCT	CCT	CAG	AGC	ACA	CTG	CCC	CAG	TTA	TTC	CTG	AAA	822
175	Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser	Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	
176				225				230					235				
178	GTG	GGG	GAA	CCC	TTG	TGG	ATC	AGG	TGT	AAG	GCC	ATC	CAT	GTG	AAC	CAT	870
179	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys	Lys	Ala	Ile	His	Val	Asn	His	
180		240					245					250					
182	GGA	TTC	GGG	CTC	ACC	TGG	GAG	CTG	GAA	GAC	AAA	GCC	CTG	GAG	GAG	GGC	918
183	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	
184		255				260					265						
186	AGC	TAC	TTT	GAG	ATG	AGT	ACC	TAC	TCC	ACA	AAC	AGG	ACC	ATG	ATT	CGG	966
187	Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	
188	270					275				280						285	
190	ATT	CTC	TTG	GCC	TTT	GTG	TCT	TCC	GTG	GGA	AGG	AAC	GAC	ACC	GGA	TAT	1014
191	Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser	Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	
192				290					295					300			
194	TAC	ACC	TGC	TCT	TCC	TCA	AAG	CAC	CCC	AGC	CAG	TCA	GCG	TTG	GTG	ACC	1062
195	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	
196				305					310				315				
198	ATC	CTA	GAA	AAA	GGG	TTT	ATA	AAC	GCT	ACC	AGC	TCG	CAA	GAA	GAG	TAT	1110
199	Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn	Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	
200		320					325					330					
202	GAA	ATT	GAC	CCG	TAC	GAA	AAG	TTC	TGC	TTC	TCA	GTC	AGG	TTT	AAA	GCG	1158
203	Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe	Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	
204		335					340				345						
206	TAC	CCA	CGA	ATC	CGA	TGC	ACG	TGG	ATC	TTC	TCT	CAA	GCC	TCA	TTT	CCT	1206
207	Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp	Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	
208	350					355					360					365	
210	TGT	GAA	CAG	AGA	GGC	CTG	GAG	GAT	GGG	TAC	AGC	ATA	TCT	AAA	TTT	TGC	1254
211	Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	

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212		370		375		380	
214	GAT CAT AAG AAC AAG CCA GGA GAG TAC ATA TTC TAT GCA GAA AAT GAT					1302	
215	Asp His Lys Asn Lys Pro Gly Glu Tyr Ile Phe Tyr Ala Glu Asn Asp						
216		385		390		395	
218	GAC GCC CAG TTC ACC AAA ATG TTC ACG CTG AAT ATA AGA AAG AAA CCT					1350	
219	Asp Ala Gln Phe Thr Lys Met Phe Thr Leu Asn Ile Arg Lys Lys Pro						
220		400		405		410	
222	CAA GTG CTA GCA AAT GCC TCA GCC AGC CAG GCG TCC TGT TCC TCT GAT					1398	
223	Gln Val Leu Ala Asn Ala Ser Ala Ser Gln Ala Ser Cys Ser Ser Asp						
224		415		420		425	
226	GGC TAC CCG CTA CCC TCT TGG ACC TGG AAG AAG TGT TCG GAC AAA TCT					1446	
227	Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys Cys Ser Asp Lys Ser						
228	430		435		440		445
230	CCC AAT TGC ACG GAG GAA ATC CCA GAA GGA GTT TGG AAT AAA AAG GCT					1494	
231	Pro Asn Cys Thr Glu Glu Ile Pro Glu Gly Val Trp Asn Lys Lys Ala						
232		450		455		460	
234	AAC AGA AAA GTG TTT GGC CAG TGG GTG TCG AGC AGT ACT CTA AAT ATG					1542	
235	Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser Ser Thr Leu Asn Met						
236		465		470		475	
238	AGT GAG GCC GGG AAA GGG CTT CTG GTC AAA TGC TGT GCG TAC AAT TCT					1590	
239	Ser Glu Ala Gly Lys Gly Leu Leu Val Lys Cys Cys Ala Tyr Asn Ser						
240		480		485		490	
242	ATG GGC ACG TCT TGC GAA ACC ATC TTT TTA AAC TCA CCA GGC CCC TTC					1638	
243	Met Gly Thr Ser Cys Glu Thr Ile Phe Leu Asn Ser Pro Gly Pro Phe						
244		495		500		505	
246	CCT TTC ATC CAA GAC AAC ATC TCC TTC TAT GCG ACC ATT GGG CTC TGT					1686	
247	Pro Phe Ile Gln Asp Asn Ile Ser Phe Tyr Ala Thr Ile Gly Leu Cys						
248	510		515		520		525
250	CTC CCC TTC ATT GTT GTT CTC ATT GTG TTG ATC TGC CAC AAA TAC AAA					1734	
251	Leu Pro Phe Ile Val Val Leu Ile Val Leu Ile Cys His Lys Tyr Lys						
252		530		535		540	
254	AAG CAA TTT AGG TAC GAG AGT CAG CTG CAG ATG ATC CAG GTG ACT GGC					1782	
255	Lys Gln Phe Arg Tyr Glu Ser Gln Leu Gln Met Ile Gln Val Thr Gly						
256		545		550		555	
258	CCC CTG GAT AAC GAG TAC TTC TAC GTT GAC TTC AGG GAC TAT GAA TAT					1830	
259	Pro Leu Asp Asn Glu Tyr Phe Tyr Val Asp Phe Arg Asp Tyr Glu Tyr						
260		560		565		570	
262	GAC CTT AAG TGG GAG TTC CCG AGA GAG AAC TTA GAG TTT GGG AAG GTC					1878	
263	Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn Leu Glu Phe Gly Lys Val						
264		575		580		585	
266	CTG GGG TCT GGC GCT TTC GGG AGG GTG ATG AAC GCC ACG GCC TAT GGC					1926	
267	Leu Gly Ser Gly Ala Phe Gly Arg Val Met Asn Ala Thr Ala Tyr Gly						
268	590		595		600		605
270	ATT AGT AAA ACG GGA GTC TCA ATT CAG GTG GCG GTG AAG ATG CTA AAA					1974	
271	Ile Ser Lys Thr Gly Val Ser Ile Gln Val Ala Val Lys Met Leu Lys						
272		610		615		620	
274	GAG AAA GCT GAC AGC TGT GAA AAA GAA GCT CTC ATG TCG GAG CTC AAA					2022	
275	Glu Lys Ala Asp Ser Cys Glu Lys Glu Ala Leu Met Ser Glu Leu Lys						
276		625		630		635	

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278	ATG	ATG	ACC	CAC	CTG	GGA	CAC	CAT	GAC	AAC	ATC	GTG	AAT	CTG	CTG	GGG	2070
279	Met	Met	Thr	His	Leu	Gly	His	His	Asp	Asn	Ile	Val	Asn	Leu	Leu	Gly	
280			640						645				650				
282	GCA	TGC	ACA	CTG	TCA	GGG	CCA	GTG	TAC	TTG	ATT	TTT	GAA	TAT	TGT	TGC	2118
283	Ala	Cys	Thr	Leu	Ser	Gly	Pro	Val	Tyr	Leu	Ile	Phe	Glu	Tyr	Cys	Cys	
284		655					660					665					
286	TAT	GGT	GAC	CTC	CTC	AAC	TAC	CTA	AGA	AGT	AAA	AGA	GAG	AAG	TTT	CAC	2166
287	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	Ser	Lys	Arg	Glu	Lys	Phe	His	
288	670					675					680					685	
290	AGG	ACA	TGG	ACA	GAG	ATT	TTT	AAG	GAA	CAT	AAT	TTC	AGT	TCT	TAC	CCT	2214
291	Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	Glu	His	Asn	Phe	Ser	Ser	Tyr	Pro	
292				690					695						700		
294	ACT	TTC	CAG	GCA	CAT	TCA	AAT	TCC	AGC	ATG	CCT	GGT	TCA	CGA	GAA	GTT	2262
295	Thr	Phe	Gln	Ala	His	Ser	Asn	Ser	Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	
296			705						710				715				
298	CAG	TTA	CAC	CCG	CCC	TTG	GAT	CAG	CTC	TCA	GGG	TTC	AAT	GGG	AAT	TCA	2310
299	Gln	Leu	His	Pro	Pro	Leu	Asp	Gln	Leu	Ser	Gly	Phe	Asn	Gly	Asn	Ser	
300			720					725				730					
302	ATT	CAT	TCT	GAA	GAT	GAG	ATT	GAA	TAT	GAA	AAC	CAG	AAG	AGG	CTG	GCA	2358
303	Ile	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	Glu	Asn	Gln	Lys	Arg	Leu	Ala	
304		735					740					745					
306	GAA	GAA	GAG	GAG	GAA	GAT	TTG	AAC	GTG	CTG	ACG	TTT	GAA	GAC	CTC	CTT	2406
307	Glu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	Phe	Glu	Asp	Leu	Leu	
308	750					755				760					765		
310	TGC	TTT	GCG	TAC	CAA	GTG	GCC	AAA	GGC	ATG	GAA	TTC	CTG	GAG	TTC	AAG	2454
311	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Glu	Phe	Lys	
312			770						775						780		
314	TCG	TGT	GTC	CAC	AGA	GAC	CTG	GCA	GCC	AGG	AAT	GTG	TTG	GTC	ACC	CAC	2502
315	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	His	
316			785						790					795			
318	GGG	AAG	GTG	GTG	AAG	ATC	TGT	GAC	TTT	GGA	CTG	GCC	CGA	GAC	ATC	CTG	2550
319	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Leu	
320			800					805				810					
322	AGC	GAC	TCC	AGC	TAC	GTC	GTC	AGG	GGC	AAC	GCA	CGG	CTG	CCG	GTG	AAG	2598
323	Ser	Asp	Ser	Ser	Tyr	Val	Val	Arg	Gly	Asn	Ala	Arg	Leu	Pro	Val	Lys	
324		815					820					825					
326	TGG	ATG	GCA	CCC	GAG	AGC	TTA	TTT	GAA	GGG	ATC	TAC	ACA	ATC	AAG	AGT	2646
327	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	Tyr	Thr	Ile	Lys	Ser	
328	830					835					840				845		
330	GAC	GTC	TGG	TCC	TAC	GGC	ATC	CTT	CTC	TGG	GAG	ATA	TTT	TCA	CTG	GGT	2694
331	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	
332				850						855					860		
334	GTG	AAC	CCT	TAC	CCT	GGC	ATT	CCT	GTC	GAC	GCT	AAC	TTC	TAT	AAA	CTG	2742
335	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala	Asn	Phe	Tyr	Lys	Leu	
336			865						870					875			
338	ATT	CAG	AGT	GGA	TTT	AAA	ATG	GAG	CAG	CCA	TTC	TAT	GCC	ACA	GAA	GGG	2790
339	Ile	Gln	Ser	Gly	Phe	Lys	Met	Glu	Gln	Pro	Phe	Tyr	Ala	Thr	Glu	Gly	
340			880					885					890				
342	ATA	TAC	TTT	GTA	ATG	CAA	TCC	TGC	TGG	GCT	TTT	GAC	TCA	AGG	AAG	CGG	2838

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]